

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(i) APPLICANT:

(A) NAME: MEDICAL RESEARCH COUNCIL

(B) STREET: 20 Park Crescent

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(E) COUNTRY: UK

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(ii) TITLE OF INVENTION: Nucleic Acid Binding Proteins

(iii) NUMBER OF SEQUENCES: 2

(iv) COMPUTER READABLE FORM:

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(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 264 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

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(A) DESCRIPTION: /desc = "Synthetic DNA"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..264

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GCA GAA GAG AAG CCT TTT CAG TGT CGA ATC TGC ATG CGT AAC TTC AGC 48
Ala Glu Glu Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser
1 5 10 15

15 GAT CGT AGT AGT CTT ACC CGC CAC ACG AGG ACC CAC ACA GGC GAG AAG 96
Asp Arg Ser Ser Leu Thr Arg His Thr Arg Thr His Thr Gly Glu Lys
20 25 30

20 CCT TTT CAG TGT CGA ATC TGC ATG CGT AAC TTC AGC AGG AGC GAT AAC 144
Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp Asn
35 40 45

CTT ACG AGA CAC CTA AGG ACC CAC ACA GGC GAG AAG CCT TTT CAG TGT 192
25 Leu Thr Arg His Leu Arg Thr His Thr Gly Glu Lys Pro Phe Gln Cys
50 55 60

CGA ATC TGC ATG CGT AAC TTC AGG CAA GCT GAT CAT CTT CAA GAG CAC 240
Arg Ile Cys Met Arg Asn Phe Arg Gln Ala Asp His Leu Gln Glu His
30 65 70 75 80

CTA AAG ACC CAC ACA GGC GAG AAG 264
Leu Lys Thr His Thr Gly Glu Lys
85

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(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Ala Glu Glu Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser
1 5 10 15

Asp Arg Ser Ser Leu Thr Arg His Thr Arg Thr His Thr Gly Glu Lys
20 25 30

Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp Asn
35 40 45

Leu Thr Arg His Leu Arg Thr His Thr Gly Glu Lys Pro Phe Gln Cys
50 55 60

Arg Ile Cys Met Arg Asn Phe Arg Gln Ala Asp His Leu Gln Glu His
65 70 75 80

Leu Lys Thr His Thr Gly Glu Lys